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OM protein - protein search, using sw model

Run on: January 30, 2002, 11:51:58 ; Search time 50.08 Seconds

(without alignments) 40.891 Million cell updates/sec

US-09-432-546-5

Perfect score: 103 SRRWPWWPKWPLI 14

Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SPTRMBEL_17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_reddent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BEST AVAILABLE COPY

| RESULT | 1 | ALIGNMENTS |
|----------|--|----------------------------|
| P71431 | | |
| ID | P71431 | PRELIMINARY; PRT; 1662 AA. |
| AC | P71431; | |
| DT | 01-FEB-1997 (TREMBREL, 02, Last sequence update) | |
| DT | 01-JUN-2001 (TREMBREL, 17, Last annotation update) | |
| DE | MOPA, GENE ENCODING MANGANESE OXIDIZING PROTEIN PRECURSOR. | |
| GN | | |
| OS | Leptothrix discophora. | |
| OC | Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; | |
| OX | Leptothrix. | |
| RN | [1] | NBBI_TAXID=89; |
| RP | SEQUENCE OF 1-1150 FROM N.A. | |
| RC | STRAINSS-1; | |
| RA | Corstjens P.L.; | |
| RL | Thesis (1993), Biochemistry, Leiden University, The Netherlands. | |
| RN | [2] | |
| RP | SEQUENCE FROM N.A. | |
| RC | STRAINSS-1; | |
| RA | Corstjens P.L.; | |
| RL | Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases. | |
| RN | [3] | |
| RP | SEQUENCE FROM N.A. | |
| RC | STRAINSS-1; | |
| RA | Corstjens P.L.A.M., de Vrind J.P.M., Goosen T., de Vrind-de Jong E.W.; | |
| RL | Geomicrobiol. J. 14:91-108(1997). | |
| RN | [4] | |
| RP | SEQUENCE FROM N.A. | |
| RC | STRAINSS-1; | |
| RA | Corstjens P.L.; | |
| RL | Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. | |
| DR | EMLB; 225774; CAR81037.1; - | |
| DR | Interpro; IPR001865; Ribosomal_S2. | |
| DR | PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1. | |
| KW | Signal. | |
| FT | SIGNAL 1 33 | POTENTIAL. |
| FT | CHAIN 34 1662 | POTENTIAL. |
| SEQUENCE | 1662 AA; 174292 MW; | 639EE238600D9246 CRC64; |

| | | | | | | | | | | | | | | | |
|----|------|------|------|--------|-------------|-------------------|--------|--------|----|------|------|------|--------|--------------------|-----------------------|
| 1 | 57 | 55.3 | 1662 | 2 | P71431 | | | | 20 | 51 | 49.5 | 1173 | 12 | Q990M1 | Q990M1 human coron |
| 2 | 56 | 54.4 | 236 | 2 | Q9kfn3 | bacillus ha | Q9kfn3 | Q9kfn3 | 21 | 51 | 49.5 | 1383 | 12 | Q84712 | Q84712 porcine epi |
| 3 | 55.5 | 53.9 | 165 | 10 | Q9SNN3 | oryza sativa | Q9SNN3 | Q9SNN3 | 22 | 50 | 49.0 | 141 | 11 | Q9CZA1 | Q9CZA1 mus musculus |
| 4 | 55.5 | 53.9 | 676 | 10 | Q9FG26 | arabidopsis | Q9FG26 | Q9FG26 | 23 | 50.5 | 49.0 | 560 | 5 | Q44626 | Q44626 caenorhabditis |
| 5 | 53.5 | 51.9 | 491 | 4 | Q9BU12 | homo sapiens | Q9BU12 | Q9BU12 | 24 | 50 | 48.5 | 83 | 2 | Q9WF1 | Q9WF1 thermotoga |
| 6 | 53 | 51.5 | 95 | 10 | Q9LQN0 | arabidopsis | Q9LQN0 | Q9LQN0 | 25 | 50 | 48.5 | 492 | 10 | Q9AV15 | Q9AV15 oryza sativa |
| 7 | 52.5 | 51.0 | 970 | 10 | Q80790 | arabidopsis | Q80790 | Q80790 | 26 | 49.5 | 48.1 | 257 | 2 | Q5624 | Q5624 yersinia en |
| 8 | 52 | 50.5 | 1231 | 10 | Q82276 | arabidopsis | Q82276 | Q82276 | 27 | 49.5 | 48.1 | 723 | 12 | Q9DCU4 | Q9DCU4 porcine epi |
| 9 | 52 | 50.5 | 157 | 5 | Q9KEB8 | arabidopsis | Q9KEB8 | Q9KEB8 | 28 | 49 | 47.6 | 159 | 2 | Q9KZT3 | Q9KZT3 caenorhabditis |
| 10 | 52 | 301 | 2 | Q915M4 | pseudomonas | Q915M4 | Q915M4 | 29 | 49 | 47.6 | 169 | 1 | Q9V9Q4 | Q9V9Q4 aeropyrum p | |
| 11 | 52 | 50.5 | 1245 | 3 | Q9YV5 | trichoderma | Q9YV5 | Q9YV5 | 30 | 49 | 47.6 | 251 | 2 | Q52853 | Q52853 bacillus su |
| 12 | 51.5 | 50.0 | 109 | 10 | Q40548 | nicotiana tabacum | Q40548 | Q40548 | 31 | 49 | 47.6 | 457 | 5 | Q19573 | Q19573 caenorhabditis |
| 13 | 51.5 | 50.0 | 196 | 10 | Q8195 | nicotiana tabacum | Q8195 | Q8195 | 32 | 49 | 47.6 | 485 | 2 | Q9ARK1 | Q9ARK1 shigella fl |
| 14 | 51.5 | 50.0 | 209 | 10 | Q8194 | nicotiana tabacum | Q8194 | Q8194 | 33 | 49 | 47.6 | 669 | 5 | Q18300 | Q18300 caenorhabditis |
| 15 | 51.5 | 50.0 | 321 | 10 | Q8528 | arabidopsis | Q8528 | Q8528 | 34 | 49 | 47.6 | 746 | 12 | Q9TH31 | Q9TH31 tt virus. o |
| 16 | 51.5 | 50.0 | 2970 | 12 | Q56073 | hepatitis g | Q56073 | Q56073 | 35 | 49 | 47.6 | 1053 | 4 | Q9VBP5 | Q9VBP5 aeropyrum p |
| 17 | 51 | 49.5 | 1173 | 12 | Q990M4 | human corona | Q990M4 | Q990M4 | 36 | 49 | 47.6 | 1487 | 5 | Q9LP00 | Q9LP00 arabidopsis |
| 18 | 51 | 49.5 | 1173 | 12 | Q990M2 | human corona | Q990M2 | Q990M2 | 37 | 48 | 46.6 | 196 | 10 | Q9RQW8 | Q9RQW8 vibrio chol |
| 19 | 49.5 | | | | | | | | 38 | 48 | 46.6 | 236 | 4 | Q9P078 | Q9P078 homo sapien |
| 20 | | | | | | | | | 39 | 48 | 46.6 | 314 | 10 | Q9RY07 | Q9RY07 arabidopsis |
| 21 | | | | | | | | | 40 | 48 | 46.6 | 947 | 10 | Q9ID18 | Q9ID18 arabidopsis |
| 22 | | | | | | | | | 41 | 48 | 46.6 | 1172 | 10 | Q9LP05 | Q9LP05 arabidopsis |
| 23 | | | | | | | | | 42 | 47.5 | 46.1 | 111 | 5 | Q18753 | Q18753 caenorhabditis |
| 24 | | | | | | | | | 43 | 47.5 | 46.1 | 752 | 2 | Q9RQW8 | Q9RQW8 vibrio chol |
| 25 | | | | | | | | | 44 | 47 | 45.6 | 752 | 2 | Q9RVQ6 | Q9RVQ6 deinococcus |
| 26 | | | | | | | | | 45 | 47 | 45.6 | 133 | 5 | Q9VX67 | Q9VX67 drosophila |

| | | Query Match | Score 57; | DB 2; | Length 166; |
|----------|--------|--|--|---|-------------------------|
| | | Best Local Similarity | 63.6%; | Pred. No. 16; | Matches 7; Conservative |
| | | 1; | Mismatches | 3; | Indels 0; |
| b | 3 | RWPKWPWKPL | 13 | | |
| b | 490 | RWHWGFWFWPV | 500 | | |
| RESULT 2 | | | | | |
| | Q9KFN3 | PRELIMINARY; | PRT; | 236 AA. | |
| | D | Q9KFN3; | ID | 09FG26 | PRELIMINARY; |
| | C | 01-OCT-2000 (TREMBLrel. 15, Created) | DT | 09FG26; | PRT; |
| | T | 01-OCT-2000 (TREMBLrel. 15, Last sequence update) | DT | 01-MAR-2001 (TREMBLrel. 16, Created) | |
| | T | 01-OCT-2000 (TREMBLrel. 15, Last annotation update) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | E | BH0446 PROTEIN. | DE | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE-LIKE. | |
| | S | Bacillus halodurans. | OS | Arabidopsis thaliana (mouse-ear cress), | |
| | C | Bacteria; Firmicutes; Bacillus/clostridium group; | OC | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | |
| | C | Bacillus/staphylococcus group; Bacillus. | OC | Spermatophyta; Magnoliophyta; euicotsyledons; core eudicots; Rosidae; | |
| | X | NCBI_TAXID=86665; | OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. | |
| | [1] | | OX | NCBI_TAXID=3702; | |
| | | SEQUENCE FROM N. A. | RN | [1]-TAXID=3702; | |
| | | STRAIN=C-125 / JCM 9153; | RC | SEQUENCE FROM N. A. | |
| | | MEDLINE=20512582; Pubmed=11058132; | RA | STRAIN=COJUMBA; | |
| | | Takami H., Nakasono K., Takaki Y., Maeno G., Sasaki R., Masui N., | RA | Kaneiro T., Katoh T., Asanizu E., Sato S., Nakamura Y., Kotani H., | |
| | | Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S., | RA | Tabata S.; | |
| | | Hokikoshi K.; | RT | "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; | |
| | | Complete genome sequence of the alkaliphilic bacterium <i>Bacillus</i> <i>Bacillus</i> subtilis.;" | RL | Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. | |
| | | Nucleic Acids Res 28:4317-4331(2000). | DR | EMBL: AP002032; BAB09815.1; | |
| | | Complete proteome; | KW | RNA-directed DNA polymerase. | |
| | | EMBL: AR001508; BAB04165.1; -. | KW | EMBL: AP002032; BAB09815.1; | |
| | | SEQUENCE 236 AA; | SQ | RNA-directed DNA polymerase. | |
| | | 26988 MW; A0BD60D9EFE34FA9 CRC64; | SQ | SEQUENCE 675 AA; 76665 MW; AD1CC1E18E46F53A CRC64; | |
| RESULT 3 | | | | | |
| | Q9NN3 | PRELIMINARY; | PRT; | 165 AA. | |
| | D | Q9NN3; | ID | 09B12 | PRELIMINARY; |
| | C | 01-MAY-2000 (TREMBLrel. 13, Created) | AC | 09B12; | PRT; |
| | T | 01-MAY-2000 (TREMBLrel. 13, Last sequence update) | DT | 01-JUN-2001 (TREMBLrel. 17, Created) | |
| | T | 01-MAY-2000 (TREMBLrel. 13, Last annotation update) | DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) | |
| | E | HYPOTHETICAL PROTEIN. | DT | 01-JUN-2001 (TREMBLrel. 17, Last annotation update) | |
| | S | Oryza sativa (Rice); | DE | SIMILAR TO FERREDOKIN REDUCTASE. | |
| | C | Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta; | OS | Homo sapiens (Human); | |
| | C | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; | OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | C | Ehretioidae; Oryzeae; Oryza. | OC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | |
| | X | NCBI_TAXID=4530; | OX | NCBI_TAXID=9606; | |
| | [1] | SEQUENCE FROM N. A. | RN | [1] | |
| | | TISSUE=LUNG CARCINOMA; | RP | SEQUENCE FROM N. A. | |
| | | Strausberg R.; | RC | TISSUE=LUNG CARCINOMA; | |
| | | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | RA | Strausberg R.; | |
| | | EMBL: BC002960; AAH02960.1; -. | RL | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | |
| | | SEQUENCE 491 AA; 53836 MW; 15D07E714F592C9D CRC64; | DR | EMBL: BC002960; AAH02960.1; -. | |
| | | SQ | SEQUENCE 491 AA; 53836 MW; 15D07E714F592C9D CRC64; | | |
| RESULT 4 | | | | | |
| | Q9FG26 | PRELIMINARY; | PRT; | 676 AA. | |
| | ID | 09FG26 | PRELIMINARY; | | |
| | AC | Q9FG26; | PRT; | | |
| | D | 01-MAR-2001 (TREMBLrel. 16, Created) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | T | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | E | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | OC | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | |
| | S | Bacillus halodurans. | OC | Spermatophyta; Magnoliophyta; euicotsyledons; core eudicots; Rosidae; | |
| | C | Nucleic Acids Res 28:4317-4331(2000). | OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. | |
| | X | Complete proteome; | OC | NCBI_TAXID=3702; | |
| | [1] | SEQUENCE FROM N. A. | RN | [1]-TAXID=3702; | |
| | | STRAIN=C-125 / JCM 9153; | RC | SEQUENCE FROM N. A. | |
| | | MEDLINE=20512582; Pubmed=11058132; | RA | STRAIN=COJUMBA; | |
| | | Takami H., Nakasono K., Takaki Y., Maeno G., Sasaki R., Masui N., | RA | Kaneiro T., Katoh T., Asanizu E., Sato S., Nakamura Y., Kotani H., | |
| | | Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S., | RA | Tabata S.; | |
| | | Hokikoshi K.; | RT | "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; | |
| | | Complete genome sequence of the alkaliphilic bacterium <i>Bacillus</i> <i>Bacillus</i> subtilis.;" | RL | Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. | |
| | | Nucleic Acids Res 28:4317-4331(2000). | DR | EMBL: AP002032; BAB09815.1; | |
| | | Complete proteome; | KW | RNA-directed DNA polymerase. | |
| | | EMBL: AR001508; BAB04165.1; -. | KW | EMBL: AP002032; BAB09815.1; | |
| | | SEQUENCE 236 AA; | SQ | RNA-directed DNA polymerase. | |
| | | 26988 MW; A0BD60D9EFE34FA9 CRC64; | SQ | SEQUENCE 675 AA; 76665 MW; AD1CC1E18E46F53A CRC64; | |
| RESULT 5 | | | | | |
| | Q9B12 | PRELIMINARY; | PRT; | 459 | |
| | ID | 09B12 | PRELIMINARY; | | |
| | AC | 09B12; | PRT; | | |
| | D | 01-JUN-2001 (TREMBLrel. 17, Created) | DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) | |
| | T | 01-JUN-2001 (TREMBLrel. 17, Last annotation update) | DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) | |
| | E | HYPOTHETICAL PROTEIN. | DT | 01-JUN-2001 (TREMBLrel. 17, Last annotation update) | |
| | S | Oryza sativa (Rice); | DE | SIMILAR TO FERREDOKIN REDUCTASE. | |
| | C | Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta; | OS | Homo sapiens (Human); | |
| | C | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; | OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | C | Ehretioidae; Oryzeae; Oryza. | OC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | |
| | X | NCBI_TAXID=4530; | OX | NCBI_TAXID=9606; | |
| | [1] | SEQUENCE FROM N. A. | RN | [1] | |
| | | TISSUE=LUNG CARCINOMA; | RP | SEQUENCE FROM N. A. | |
| | | Strausberg R.; | RC | TISSUE=LUNG CARCINOMA; | |
| | | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | RA | Strausberg R.; | |
| | | EMBL: BC002960; AAH02960.1; -. | RL | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | |
| | | SEQUENCE 491 AA; 53836 MW; 15D07E714F592C9D CRC64; | DR | EMBL: BC002960; AAH02960.1; -. | |
| | | SQ | SEQUENCE 491 AA; 53836 MW; 15D07E714F592C9D CRC64; | | |
| RESULT 6 | | | | | |
| | Q9FG32 | PRELIMINARY; | PRT; | 676 AA. | |
| | ID | 09FG32 | PRELIMINARY; | | |
| | AC | Q9FG32; | PRT; | | |
| | D | 01-MAR-2001 (TREMBLrel. 16, Created) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | T | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | E | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | OC | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | |
| | S | Bacillus halodurans. | OC | Spermatophyta; Magnoliophyta; euicotsyledons; core eudicots; Rosidae; | |
| | C | Nucleic Acids Res 28:4317-4331(2000). | OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. | |
| | X | Complete proteome; | OC | NCBI_TAXID=3702; | |
| | [1] | SEQUENCE FROM N. A. | RN | [1]-TAXID=3702; | |
| | | STRAIN=C-125 / JCM 9153; | RC | SEQUENCE FROM N. A. | |
| | | MEDLINE=20512582; Pubmed=11058132; | RA | STRAIN=COJUMBA; | |
| | | Takami H., Nakasono K., Takaki Y., Maeno G., Sasaki R., Masui N., | RA | Kaneiro T., Katoh T., Asanizu E., Sato S., Nakamura Y., Kotani H., | |
| | | Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S., | RA | Tabata S.; | |
| | | Hokikoshi K.; | RT | "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; | |
| | | Complete genome sequence of the alkaliphilic bacterium <i>Bacillus</i> <i>Bacillus</i> subtilis.;" | RL | Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. | |
| | | Nucleic Acids Res 28:4317-4331(2000). | DR | EMBL: AP002032; BAB09815.1; | |
| | | Complete proteome; | KW | RNA-directed DNA polymerase. | |
| | | EMBL: AR001508; BAB04165.1; -. | KW | EMBL: AP002032; BAB09815.1; | |
| | | SEQUENCE 236 AA; | SQ | RNA-directed DNA polymerase. | |
| | | 26988 MW; A0BD60D9EFE34FA9 CRC64; | SQ | SEQUENCE 675 AA; 76665 MW; AD1CC1E18E46F53A CRC64; | |
| RESULT 7 | | | | | |
| | Q9FG33 | PRELIMINARY; | PRT; | 676 AA. | |
| | ID | 09FG33 | PRELIMINARY; | | |
| | AC | Q9FG33; | PRT; | | |
| | D | 01-MAR-2001 (TREMBLrel. 16, Created) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | T | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | E | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | OC | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | |
| | S | Bacillus halodurans. | OC | Spermatophyta; Magnoliophyta; euicotsyledons; core eudicots; Rosidae; | |
| | C | Nucleic Acids Res 28:4317-4331(2000). | OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. | |
| | X | Complete proteome; | OC | NCBI_TAXID=3702; | |
| | [1] | SEQUENCE FROM N. A. | RN | [1]-TAXID=3702; | |
| | | STRAIN=C-125 / JCM 9153; | RC | SEQUENCE FROM N. A. | |
| | | MEDLINE=20512582; Pubmed=11058132; | RA | STRAIN=COJUMBA; | |
| | | Takami H., Nakasono K., Takaki Y., Maeno G., Sasaki R., Masui N., | RA | Kaneiro T., Katoh T., Asanizu E., Sato S., Nakamura Y., Kotani H., | |
| | | Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S., | RA | Tabata S.; | |
| | | Hokikoshi K.; | RT | "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; | |
| | | Complete genome sequence of the alkaliphilic bacterium <i>Bacillus</i> <i>Bacillus</i> subtilis.;" | RL | Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. | |
| | | Nucleic Acids Res 28:4317-4331(2000). | DR | EMBL: AP002032; BAB09815.1; | |
| | | Complete proteome; | KW | RNA-directed DNA polymerase. | |
| | | EMBL: AR001508; BAB04165.1; -. | KW | EMBL: AP002032; BAB09815.1; | |
| | | SEQUENCE 236 AA; | SQ | RNA-directed DNA polymerase. | |
| | | 26988 MW; A0BD60D9EFE34FA9 CRC64; | SQ | SEQUENCE 675 AA; 76665 MW; AD1CC1E18E46F53A CRC64; | |
| RESULT 8 | | | | | |
| | Q9FG34 | PRELIMINARY; | PRT; | 676 AA. | |
| | ID | 09FG34 | PRELIMINARY; | | |
| | AC | Q9FG34; | PRT; | | |
| | D | 01-MAR-2001 (TREMBLrel. 16, Created) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | T | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | E | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | OC | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | |
| | S | Bacillus halodurans. | OC | Spermatophyta; Magnoliophyta; euicotsyledons; core eudicots; Rosidae; | |
| | C | Nucleic Acids Res 28:4317-4331(2000). | OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. | |
| | X | Complete proteome; | OC | NCBI_TAXID=3702; | |
| | [1] | SEQUENCE FROM N. A. | RN | [1]-TAXID=3702; | |
| | | STRAIN=C-125 / JCM 9153; | RC | SEQUENCE FROM N. A. | |
| | | MEDLINE=20512582; Pubmed=11058132; | RA | STRAIN=COJUMBA; | |
| | | Takami H., Nakasono K., Takaki Y., Maeno G., Sasaki R., Masui N., | RA | Kaneiro T., Katoh T., Asanizu E., Sato S., Nakamura Y., Kotani H., | |
| | | Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S., | RA | Tabata S.; | |
| | | Hokikoshi K.; | RT | "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; | |
| | | Complete genome sequence of the alkaliphilic bacterium <i>Bacillus</i> <i>Bacillus</i> subtilis.;" | RL | Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. | |
| | | Nucleic Acids Res 28:4317-4331(2000). | DR | EMBL: AP002032; BAB09815.1; | |
| | | Complete proteome; | KW | RNA-directed DNA polymerase. | |
| | | EMBL: AR001508; BAB04165.1; -. | KW | EMBL: AP002032; BAB09815.1; | |
| | | SEQUENCE 236 AA; | SQ | RNA-directed DNA polymerase. | |
| | | 26988 MW; A0BD60D9EFE34FA9 CRC64; | SQ | SEQUENCE 675 AA; 76665 MW; AD1CC1E18E46F53A CRC64; | |
| RESULT 9 | | | | | |
| | Q9FG35 | PRELIMINARY; | PRT; | 676 AA. | |
| | ID | 09FG35 | PRELIMINARY; | | |
| | AC | Q9FG35; | PRT; | | |
| | D | 01-MAR-2001 (TREMBLrel. 16, Created) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | T | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | |
| | E | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | OC | Bukayota; Vidioplanteae; Streptophyta; Embryophyta; | |
| | S | Bacillus halodurans. | OC | Spermatophyta; Magnoliophyta; euicotsyledons; core eudicots; Rosidae; | |
| | C | Nucleic Acids Res 28:4317-4331(2000). | OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. | |
| | X | Complete proteome; | OC | NCBI_TAXID=3702; | |
| | [1] | SEQUENCE FROM N. A. | RN | [1]-TAXID=3702; | |
| | | STRAIN=C-125 / JCM 9153; | RC | SEQUENCE FROM N. A. | |
| | | MEDLINE=20512582; Pubmed=11058132; | RA | STRAIN=COJUMBA; | |
| | | Takami H., Nakasono K., Takaki Y., Maeno G., Sasaki R., Masui N., | RA | Kaneiro T., Katoh T., Asanizu E., Sato S., Nakamura Y., Kotani H., | |
| | | Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S., | RA | Tabata S.; | |
| | | Hokikoshi K.; | RT | "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; | |
| | | Complete genome sequence of the alkaliphilic bacterium <i>Bacillus</i> <i>Bacillus</i> subtilis.;" | RL | Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. | |
| | | Nucleic Acids Res 28:4317-4331(2000). | DR | EMBL: AP002032; BAB09815.1; | |
| | | Complete proteome; | KW | RNA-directed DNA polymerase. | |
| | | EMBL: AR001508; BAB04165.1; -. | KW | EMBL: AP002032; BAB09815.1; | |
| | | SEQUENCE 236 AA; | SQ | RNA-directed DNA polymerase. | |
| | | 26988 MW; A0BD60D9EFE34FA9 CRC64; | SQ | SEQUENCE 675 AA; 76665 MW; AD1CC1E18E46F53A CRC64; | |

| RESULT | 13 | POTENTIAL. | | | | | | | | | | | | | | | | | | |
|--------|---|---|------|---------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| ID | Q08195 | PRELIMINARY; | PRT; | 196 AA. | PLISTIL-SPECIFIC EXTENSION-LIKE PROTEIN. | | | | | | | | | | | | | | | |
| AC | Q08195; | | | | 5 X AA REPEATS OF S-P(4). | | | | | | | | | | | | | | | |
| DT | 01-Nov-1996 | (TREMBLrel. 01, created) | | | 1. | | | | | | | | | | | | | | | |
| DT | 01-Nov-1996 | (TREMBLrel. 01, last sequence update) | | | 2. | | | | | | | | | | | | | | | |
| DR | 01-JUN-2006 | (TREMBLrel. 14, last annotation update) | | | 4. | | | | | | | | | | | | | | | |
| DE | CYSTEINE-RICH EXTENSION-LIKE PROTEIN 2. | | | | | | | | | | | N-LINKED (GLCNAC- . -) (POTENTIAL). | | | | | | | | |
| OS | Nicotiana tabacum (Common tobacco). | | | | | | | | | | | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | | | | | | |
| OC | Spermato phyta; Magnoliophyta; eudicots; core eudicots; | | | | | | | | | | | Asterales; eudicots I; Solanales; Solanaceae; Nicotiana. | | | | | | | | |
| OC | NCBI_TaxID=4097; | | | | | | | | | | | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | | | | MEDLINE=93342083; PubMed=8341705; | | | | | | | | |
| RX | Wu H.M., Zou J., May B., Gu Q., Cheung A.Y.; "A tobacco gene family for flower cell wall proteins with a proline-rich domain and a cysteine-rich domain"; Proc. Natl. Acad. Sci. U.S.A. 90:6829-6833(1993). | | | | | | | | | | | [2] | | | | | | | | |
| RT | SEQUENCE OF 39-209 FROM N.A. | | | | | | | | | | | SEQUENCE FROM N.A. | | | | | | | | |
| RT | MEDLINE=93005740; PubMed=1392607; | | | | | | | | | | | MEDLINE=9-3342083; PubMed=8341705; | | | | | | | | |
| RT | Goldman S., Pezzotti M., Seurinck J., Mariani C.; "Developmental expression of tobacco pistil-specific genes encoding novel extensin-like proteins. "; Plant Cell 4:1041-1051(1992). | | | | | | | | | | | [1] | | | | | | | | |
| RT | "- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE); DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER POLLINATION. | | | | | | | | | | | Search completed: January 30, 2002, 11:51:58 | | | | | | | | |
| CC | EMBL; Li3439; AAC34059.1; "- | | | | | | | | | | | Job time: 197 sec | | | | | | | | |
| CC | EMBL; Z14020; CAA78388.1; "- | | | | | | | | | | | Mendel; 16901; Nicta2747; 16901. | | | | | | | | |
| CC | Structural protein; Repeat; Glycoprotein; Signal. | | | | | | | | | | | [1] | | | | | | | | |
| RESULT | 14 | POTENTIAL. | | | | | | | | | | SEQUENCE FROM N.A. | | | | | | | | |
| ID | Q08194 | PRELIMINARY; | PRT; | 209 AA. | MEDLINE=93342083; PubMed=8341705; | | | | | | | | | | | | | | | |
| AC | Q08194; | | | | Query Match Best Local Similarity 50.0%; Score 51.5; DB 10; Length 196; Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1; | | | | | | | RT | | | | | | | | |
| DT | 01-JAN-1998 | (TREMBLrel. 05, Created) | | | RT | | | | | | | | | | | | | | | |
| DT | 01-JUN-2000 | (TREMBLrel. 14, Last annotation update) | | | RT | | | | | | | RT | | | | | | | | |
| DE | PISTIL-SPECIFIC EXTENSION-LIKE PROTEIN PRECURSOR (CYSTEINE-RICH EXTENSION-LIKE PROTEIN 1). | | | | | | | | | | | RT | | | | | | | | |
| GN | (Cysteine-Rich Extensin-Like Protein 1). | | | | | | | | | | | RT | | | | | | | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | | | | | | | | | | RT | | | | | | | | |
| OC | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermato phyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. | | | | | | | | | | | RT | | | | | | | | |
| OX | NCBI_TaxID=3702; | | | | | | | | | | | RN | | | | | | | | |
| RN | [1] | | | | | | | | | | | SEQUENCE FROM N.A. | | | | | | | | |
| RC | RT | | | | | | | | | | | RT | | | | | | | | |
| RX | STRAIN=CV. COLUMBIA; | | | | | | | | | | | RT | | | | | | | | |
| RA | MEDLINE=20083487; PubMed=10617197; | | | | | | | | | | | RT | | | | | | | | |
| RA | Lin X., Kaul S., Rounseley S.D., Shear T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason C.L., Barnstead M.E., Feldblum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Ohayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D., Nieman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C., Nature 403:761-768(1999), EMBL; AC00592; AAB2368.1; -. | | | | | | | | | | | RT | | | | | | | | |
| RA | Ra | | | | | | | | | | | RT | | | | | | | | |
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